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RAW SEQUENCE LISTING

DATE: 10/09/2001

PATENT APPLICATION: US/09/955,866

TIME: 09:30:19

Input Set : A:\00759Aseq.txt

Output Set: N:\CRF3\10092001\I955866.raw

0590
1015

2

ENTERED

p. 5

```

3 <110> APPLICANT: Fox, Michael
4     Sullivan, John K.
5     Holst, Paige
6     Yoshinaga, Steven Kiyoshi
8 <120> TITLE OF INVENTION: B7-Like Polypeptides and Uses Thereof
10 <130> FILE REFERENCE: 00,759-A
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/955,866
C--> 13 <141> CURRENT FILING DATE: 2001-09-19
15 <150> PRIOR APPLICATION NUMBER: 60/233,867
16 <151> PRIOR FILING DATE: 2000-09-20
18 <160> NUMBER OF SEQ ID NOS: 30
20 <170> SOFTWARE: PatentIn Ver. 2.0
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 1209
24 <212> TYPE: DNA
25 <213> ORGANISM: Homo sapiens
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28 <221> NAME/KEY: CDS
29 <222> LOCATION: (33)..(854)
31 <220> FEATURE:
32 <221> NAME/KEY: sig_peptide
33 <222> LOCATION: (33)..(89)
35 <220> FEATURE:
36 <221> NAME/KEY: misc_feature
37 <222> LOCATION: (693)..(755)
38 <223> OTHER INFORMATION: predicted transmembrane domain
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42                               Met Ile Phe Leu Leu Met
43                               1           5
45 ttg agc ctg gaa ttg cag ott cac cag ata gca gct tta ttc aca gtg   101
46 Leu Ser Leu Glu Leu Gln Leu His Gln Ile Ala Ala Leu Phe Thr Val
47       10           15           20
49 aca gtc cct aag gaa ctg tac ata ata gag cat ggc agc aat gtg acc   149
50 Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu His Gly Ser Asn Val Thr
51       25           30           35
53 ctg gaa tgc aac ttt gac act gga agt cat gtg aac ctt gga gca ata   197
54 Leu Glu Cys Asn Phe Asp Thr Gly Ser His Val Asn Leu Gly Ala Ile
55 40           45           50           55
57 aca gcc agt ttg caa aag gtg gaa aat gat aca tcc cca cac cgt gaa   245
58 Thr Ala Ser Leu Gln Lys Val Glu Asn Asp Thr Ser Pro His Arg Glu
59       60           65           70
61 aga gcc act ttg ctg gag gag cag ctg ccc cta ggg aag gcc tcg ttc   293
62 Arg Ala Thr Leu Leu Glu Glu Gln Leu Pro Leu Gly Lys Ala Ser Phe
63       75           80           85
65 cac ata cct caa gtc caa gtg agg gac gaa gga cag tac caa tgc ata   341
66 His Ile Pro Gln Val Gln Val Arg Asp Glu Gly Gln Tyr Gln Cys Ile

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67          90          95          100
69 atc atc tat ggg gtc gcc tgg gac tac aag tac ctg act ctg aaa gtc 389
70 Ile Ile Tyr Gly Val Ala Trp Asp Tyr Lys Tyr Leu Thr Leu Lys Val
71      105      110      115
73 aaa gct tcc tac agg aaa ata aac act cac atc cta aag gtt cca gaa 437
74 Lys Ala Ser Tyr Arg Lys Ile Asn Thr His Ile Leu Lys Val Pro Glu
75 120      125      130      135
77 aca gat gag gta gag ctc acc tgc cag gct aca ggt tat cct ctg gca 485
78 Thr Asp Glu Val Glu Leu Thr Cys Gln Ala Thr Gly Tyr Pro Leu Ala
79      140      145      150
81 gaa gta tcc tgg cca aac gtc agc gtt cct gcc aac acc agc cac tcc 533
82 Glu Val Ser Trp Pro Asn Val Ser Val Pro Ala Asn Thr Ser His Ser
83      155      160      165
85 agg acc cct gaa ggc ctc tac cag gtc acc agt gtt ctg cgc cta aag 581
86 Arg Thr Pro Glu Gly Leu Tyr Gln Val Thr Ser Val Leu Arg Leu Lys
87      170      175      180
89 cca ccc cct ggc aga aac ttc agc tgt gtg ttc tgg aat act cac gtg 629
90 Pro Pro Pro Gly Arg Asn Phe Ser Cys Val Phe Trp Asn Thr His Val
91      185      190      195
93 agg gaa ctt act ttg gcc agc att gac ctt caa agt cag atg gaa ccc 677
94 Arg Glu Leu Thr Leu Ala Ser Ile Asp Leu Gln Ser Gln Met Glu Pro
95 200      205      210      215
97 agg acc cat cca act tgg ctg ctt cac att ttc atc ccc tcc tgc atc 725
98 Arg Thr His Pro Thr Trp Leu Leu His Ile Phe Ile Pro Ser Cys Ile
99      220      225      230
101 att gct ttc att ttc ata gcc aca gtg ata gcc cta aga aaa caa ctc 773
102 Ile Ala Phe Ile Phe Ile Ala Thr Val Ile Ala Leu Arg Lys Gln Leu
103      235      240      245
105 tgt caa aag ctg tat tct tca aaa gac aca aca aaa aga cct gtc acc 821
106 Cys Gln Lys Leu Tyr Ser Ser Lys Asp Thr Thr Lys Arg Pro Val Thr
107      250      255      260
109 aca aca aag agg gaa gtg aac agt gct atc tga acctgtgggtc ttgggagcca 874
110 Thr Thr Lys Arg Glu Val Asn Ser Ala Ile
111      265      270
113 ggggtgacctg atatgacatc taaagaagct tctggactct gaacaagaat tcggtggcct 934
115 gcagagcttg ccatttgac ttttcaaagt cctttggatg acccagcact ttaatctgaa 994
117 acctgcaaca agactagcca acacctggcc atgaaacttg ccccttcact gatctggact 1054
119 caccctctgga gcctatggct ttaagcaagc actactgcac ttacagaat taccctactg 1114
121 gatcctggac ccacagaatt ccttcaggat ccttcttgct gccagactga aagcaaaagg 1174
123 aattatttcc cctcaagttt tctaagtgat ttcca 1209
126 <210> SEQ ID NO: 2
127 <211> LENGTH: 273
128 <212> TYPE: PRT
129 <213> ORGANISM: Homo sapiens
131 <400> SEQUENCE: 2
132 Met Ile Phe Leu Leu Met Leu Ser Leu Glu Leu Gln Leu His Gln
133 1 5 10 15
135 Ile Ala Ala Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile
136 20 25 30

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138 Glu His Gly Ser Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser
139           35                      40                      45
141 His Val Asn Leu Gly Ala Ile Thr Ala Ser Leu Gln Lys Val Glu Asn
142           50                      55                      60
144 Asp Thr Ser Pro His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu
145           65                      70                      75                      80
147 Pro Leu Gly Lys Ala Ser Phe His Ile Pro Gln Val Gln Val Arg Asp
148           85                      90                      95
150 Glu Gly Gln Tyr Gln Cys Ile Ile Ile Tyr Gly Val Ala Trp Asp Tyr
151           100                     105                     110
153 Lys Tyr Leu Thr Leu Lys Val Lys Ala Ser Tyr Arg Lys Ile Asn Thr
154           115                     120                     125
156 His Ile Leu Lys Val Pro Glu Thr Asp Glu Val Glu Leu Thr Cys Gln
157           130                     135                     140
159 Ala Thr Gly Tyr Pro Leu Ala Glu Val Ser Trp Pro Asn Val Ser Val
160           145                     150                     155                      160
162 Pro Ala Asn Thr Ser His Ser Arg Thr Pro Glu Gly Leu Tyr Gln Val
163           165                     170                     175
165 Thr Ser Val Leu Arg Leu Lys Pro Pro Pro Gly Arg Asn Phe Ser Cys
166           180                     185                     190
168 Val Phe Trp Asn Thr His Val Arg Glu Leu Thr Leu Ala Ser Ile Asp
169           195                     200                     205
171 Leu Gln Ser Gln Met Glu Pro Arg Thr His Pro Thr Trp Leu Leu His
172           210                     215                     220
174 Ile Phe Ile Pro Ser Cys Ile Ile Ala Phe Ile Phe Ile Ala Thr Val
175           225                     230                     235                      240
177 Ile Ala Leu Arg Lys Gln Leu Cys Gln Lys Leu Tyr Ser Ser Lys Asp
178           245                     250                     255
180 Thr Thr Lys Arg Pro Val Thr Thr Thr Lys Arg Glu Val Asn Ser Ala
181           260                     265                     270
183 Ile
186 <210> SEQ ID NO: 3
187 <211> LENGTH: 254
188 <212> TYPE: PRT
189 <213> ORGANISM: Homo sapiens
191 <220> FEATURE:
192 <221> NAME/KEY: TRANSMEM
193 <222> LOCATION: (202)..(222)
195 <400> SEQUENCE: 3
196 Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu His Gly
197           1           5           10           15
199 Ser Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser His Val Asn
200           20           25           30
202 Leu Gly Ala Ile Thr Ala Ser Leu Gln Lys Val Glu Asn Asp Thr Ser
203           35           40           45
205 Pro His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu Pro Leu Gly
206           50           55           60
208 Lys Ala Ser Phe His Ile Pro Gln Val Gln Val Arg Asp Glu Gly Gln
209           65           70           75           80

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211 Tyr Gln Cys Ile Ile Ile Tyr Gly Val Ala Trp Asp Tyr Lys Tyr Leu
212                               85                               90                               95
214 Thr Leu Lys Val Lys Ala Ser Tyr Arg Lys Ile Asn Thr His Ile Leu
215                               100                               105                               110
217 Lys Val Pro Glu Thr Asp Glu Val Glu Leu Thr Cys Gln Ala Thr Gly
218                               115                               120                               125
220 Tyr Pro Leu Ala Glu Val Ser Trp Pro Asn Val Ser Val Pro Ala Asn
221                               130                               135                               140
223 Thr Ser His Ser Arg Thr Pro Glu Gly Leu Tyr Gln Val Thr Ser Val
224 145                               150                               155                               160
226 Leu Arg Leu Lys Pro Pro Gly Arg Asn Phe Ser Cys Val Phe Trp
227                               165                               170                               175
229 Asn Thr His Val Arg Glu Leu Thr Leu Ala Ser Ile Asp Leu Gln Ser
230                               180                               185                               190
232 Gln Met Glu Pro Arg Thr His Pro Thr Trp Leu Leu His Ile Phe Ile
233                               195                               200                               205
235 Pro Ser Cys Ile Ile Ala Phe Ile Phe Ile Ala Thr Val Ile Ala Leu
236 210                               215                               220
238 Arg Lys Gln Leu Cys Gln Lys Leu Tyr Ser Ser Lys Asp Thr Thr Lys
239 225                               230                               235                               240
241 Arg Pro Val Thr Thr Thr Lys Arg Glu Val Asn Ser Ala Ile
242                               245                               250
245 <210> SEQ ID NO: 4
246 <211> LENGTH: 224
247 <212> TYPE: PRT
248 <213> ORGANISM: Homo sapiens
250 <400> SEQUENCE: 4
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252 1                               5                               10                               15
254 Leu Asn Phe Phe Gln Leu Leu Val Leu Ala Gly Leu Ser His Phe Cys
255                               20                               25                               30
257 Ser Gly Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu
258 35                               40                               45
260 Ser Cys Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile
261 50                               55                               60
263 Tyr Trp Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp
264 65                               70                               75                               80
266 Met Asn Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr
267                               85                               90                               95
269 Asn Asn Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly
270 100                               105                               110
272 Thr Tyr Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg
273 115                               120                               125
275 Glu His Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr
276 130                               135                               140
278 Pro Ser Ile Ser Asp Phe Glu Ile Pro Thr Ser Asn Ile Arg Arg Ile
279 145                               150                               155                               160
281 Ile Cys Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu
282                               165                               170                               175

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284 Glu Asn Gly Glu Glu Leu Asn Ala Ile Asn Thr Thr Val Ser Gln Asp
285          180          185          190
287 Pro Glu Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met
288          195          200          205
290 Thr Thr Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg
291          210          215          220
297 <210> SEQ ID NO: 5
298 <211> LENGTH: 323
299 <212> TYPE: PRT
300 <213> ORGANISM: Homo sapiens
302 <400> SEQUENCE: 5
303 Met Gly Leu Ser Asn Ile Leu Phe Val Met Ala Phe Leu Leu Ser Gly
304   1          5          10          15
306 Ala Ala Pro Leu Lys Ile Gln Ala Tyr Phe Asn Glu Thr Ala Asp Leu
307          20          25          30
309 Pro Cys Gln Phe Ala Asn Ser Gln Asn Gln Ser Leu Ser Glu Leu Val
310          35          40          45
312 Val Phe Trp Gln Asp Gln Glu Asn Leu Val Leu Asn Glu Val Tyr Leu
313          50          55          60
315 Gly Lys Glu Lys Phe Asp Ser Val His Ser Lys Tyr Met Gly Arg Thr
316   65          70          75          80
318 Ser Phe Asp Ser Asp Ser Trp Thr Leu Arg Leu His Asn Leu Gln Ile
319          85          90          95
321 Lys Asp Lys Gly Leu Tyr Gln Cys Ile Ile His His Lys Lys Pro Thr
322          100          105          110
324 Gly Met Ile Arg Ile His Gln Met Asn Ser Glu Leu Ser Val Leu Ala
325          115          120          125
327 Asn Phe Ser Gln Pro Glu Ile Val Pro Ile Ser Asn Ile Thr Glu Asn
328          130          135          140
330 Val Tyr Ile Asn Leu Thr Cys Ser Ser Ile His Gly Tyr Pro Glu Pro
331 145          150          155          160
333 Lys Lys Met Ser Val Leu Leu Arg Thr Lys Asn Ser Thr Ile Glu Tyr
334          165          170          175
336 Asp Gly Ile Met Gln Lys Ser Gln Asp Asn Val Thr Glu Leu Tyr Asp
337          180          185          190
339 Val Ser Ile Ser Leu Ser Val Ser Phe Pro Asp Val Thr Ser Asn Met
340          195          200          205
342 Thr Ile Phe Cys Ile Leu Glu Thr Asp Lys Thr Arg Leu Leu Ser Ser
343          210          215          220
345 Pro Phe Ser Ile Glu Leu Glu Asp Pro Gln Pro Pro Pro Asp His Ile
346 225          230          235          240
348 Pro Trp Ile Thr Ala Val Leu Pro Thr Val Ile Ile Cys Val Met Val
349          245          250          255
351 Phe Cys Leu Ile Leu Trp Lys Trp Lys Lys Lys Lys Arg Pro Arg Asn
352          260          265          270
354 Ser Tyr Lys Cys Gly Thr Asn Thr Met Glu Arg Glu Glu Ser Glu Gln
355          275          280          285
357 Thr Lys Lys Arg Glu Lys Ile His Ile Pro Glu Arg Ser Asp Glu Ala
358          290          295          300

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Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY

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Input Set : A:\00759Aseq.txt

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L:12 M:270 C: Current Application Number differs, Replaced Application Number
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:548 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:1086 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1088 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1090 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1146 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1148 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1150 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1152 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1154 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1156 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1158 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1160 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1162 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1164 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1166 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1168 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1170 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1172 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1174 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1176 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1178 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1180 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1182 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1184 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1186 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1188 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1190 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1192 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1194 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1198 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1286 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1288 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1310 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
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L:1322 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1324 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1326 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1328 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1334 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1338 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1356 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:1358 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:1360 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:1484 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:1486 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16

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L:1488 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:1492 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:1494 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:1496 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16